

SEQUENCE LISTING

- <110> Genentech, Inc.
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- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
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- <140> 09/665,350
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- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20944
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<211> 353

<212> PRT

<213> Homo sapiens

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 20 25 30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
 35 40 45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
 65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
 115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
 130 135 140

F00120"02000

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

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aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
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ggcgccttccc tgcgcgcgcgc ctctggctct ggagcatcct cctgtgcctg ctggcactgc 300
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<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

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 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

T00120" E22055

65	70	75	80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln	85	90	95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly	100	105	110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro	115	120	125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln	130	135	140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu	145	150	155
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr	165	170	175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys	180	185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His	195	200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys	210	215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn	225	230	235
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys	245	250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln	260	265	270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys	275	280	285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu	290	295	300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys	305	310	315
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His	325	330	335
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala	340	345	350

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<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
 aaagacgcat ctgcgagtgt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 10
 tgctgatttc acactgctct ccc 23

<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
 20 25 30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
 35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
 50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
 85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
 130 135 140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
 145 150 155 160

His Asp Pro Gly

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<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (33)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (80)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (94)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (144)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (188)
 <223> a, t, c or g

<400> 13
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 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
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 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420
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<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

<213> Homo sapiens

<400> 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 19

tgctgtgcta ctctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Homo sapiens

<400> 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 24

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28

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gccca

24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

<400> 26
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41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaaccccca 180
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 32

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<211> 3449

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
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Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
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Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
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Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
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Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
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Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
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Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
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Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

FOR 22063

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 38

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<212> DNA

<213> Homo sapiens

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tttgtatgaa aaa

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1813

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gtgaaatagc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
 ctaattgcac taacacagaa ggaagtatt attgtatgtg tgtacctggc ttcagatcca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaa 420
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
 taggttacaa gaacaacact atctcagcca aggacacct ttctaactca actcttactg 600
 aatttgtaaa aaccgtgaat aattttgttc aaagggatag atttgtagtt tgggacaagt 660
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
 ctttaaggat atcccagagc ttccaaaaga ccacagaggt tgatacaaat tcaacggata 780
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
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 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960
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 atgctttcca ggggatgttc atttttttat tctgtgtgt tttatctaga aagattcaag 2040
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
 agagaatggt ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160

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<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
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Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
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Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
35 40 45

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
130 135 140

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val 195 200 205		
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys 210 215 220		
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe 225 230 235 240		
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys 245 250 255		
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met 260 265 270		
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala 275 280 285		
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser 290 295 300		
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln 305 310 315 320		
Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile 325 330 335		
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys 340 345 350		
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser 355 360 365		
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp 370 375 380		
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser 385 390 395 400		
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly 405 410 415		
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln 420 425 430		
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr 435 440 445		
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys 450 455 460		

PDB ID: 1A29

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
485 490 495

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50

<211> 589

'<212> DNA

<213> Homo sapiens

<220>

<221> modified base

<222> (61)

<400> 50'

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
cqctaagcga ggcctcctcc tccgcagat ccgaacggcc tgggcggggg cccccgggct 120

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtcggt gacaagccca aa

22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggtatatt tagcctgcaa 240
 aaccccaaag aagactgttt cctccagatt agagtggag aaactgggtc ggagtgtctc 300
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360
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 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
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 acccgaggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggttaa 1200
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

305

310

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcggtgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
 aaataaatga attactcaat ctctatgac catctatata tactccacct tcaaaaagta 240
 catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300
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aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggg 600
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

000034 0400
 40020 220000

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

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<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
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 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255
 Thr Val Val

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr
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Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
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Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
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Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
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Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
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Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
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Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
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Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
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His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
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Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
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00004-0104

580

585

590

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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

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<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

22

<211> 23

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

23

<211> 50

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<211> 22

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

22

<211> 24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<210> 82

<211> 50
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 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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<210> 83
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 <212> DNA
 <213> Homo sapiens

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 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
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 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
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 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
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 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
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Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
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Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
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Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
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His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
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Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

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22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

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<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87

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<210> 88

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88

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<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
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Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
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 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
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 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
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 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
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 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
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 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

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Asn	Lys	Ile	His	Ser	Ile	Arg	Lys	Ser	His	Phe	Val	Asp	Tyr	Lys	Asn
385							390				395				400
Leu	Ile	Leu	Leu	Asp	Leu	Gly	Asn	Asn	Asn	Ile	Ala	Thr	Val	Glu	Asn
				405					410					415	
Asn	Thr	Phe	Lys	Asn	Leu	Leu	Asp	Leu	Arg	Trp	Leu	Tyr	Met	Asp	Ser
			420					425					430		
Asn	Tyr	Leu	Asp	Thr	Leu	Ser	Arg	Glu	Lys	Phe	Ala	Gly	Leu	Gln	Asn
		435					440					445			
Leu	Glu	Tyr	Leu	Asn	Val	Glu	Tyr	Asn	Ala	Ile	Gln	Leu	Ile	Leu	Pro
	450					455					460				
Gly	Thr	Phe	Asn	Ala	Met	Pro	Lys	Leu	Arg	Ile	Leu	Ile	Leu	Asn	Asn
465					470					475					480
Asn	Leu	Leu	Arg	Ser	Leu	Pro	Val	Asp	Val	Phe	Ala	Gly	Val	Ser	Leu
				485					490					495	
Ser	Lys	Leu	Ser	Leu	His	Asn	Asn	Tyr	Phe	Met	Tyr	Leu	Pro	Val	Ala
			500					505					510		
Gly	Val	Leu	Asp	Gln	Leu	Thr	Ser	Ile	Ile	Gln	Ile	Asp	Leu	His	Gly
		515					520					525			
Asn	Pro	Trp	Glu	Cys	Ser	Cys	Thr	Ile	Val	Pro	Phe	Lys	Gln	Trp	Ala
	530					535					540				
Glu	Arg	Leu	Gly	Ser	Glu	Val	Leu	Met	Ser	Asp	Leu	Lys	Cys	Glu	Thr
545					550					555					560
Pro	Val	Asn	Phe	Phe	Arg	Lys	Asp	Phe	Met	Leu	Leu	Ser	Asn	Asp	Glu
				565					570					575	
Ile	Cys	Pro	Gln	Leu	Tyr	Ala	Arg	Ile	Ser	Pro	Thr	Leu	Thr	Ser	His
			580					585					590		
Ser	Lys	Asn	Ser	Thr	Gly	Leu	Ala	Glu	Thr	Gly	Thr	His	Ser	Asn	Ser
		595					600					605			
Tyr	Leu	Asp	Thr	Ser	Arg	Val	Ser	Ile	Ser	Val	Leu	Val	Pro	Gly	Leu
	610					615					620				
Leu	Leu	Val	Phe	Val	Thr	Ser	Ala	Phe	Thr	Val	Val	Gly	Met	Leu	Val
625					630					635					640
Phe	Ile	Leu	Arg	Asn	Arg	Lys	Arg	Ser	Lys	Arg	Arg	Asp	Ala	Asn	Ser
				645					650					655	
Ser	Ala	Ser	Glu	Ile	Asn	Ser	Leu	Gln	Thr	Val	Cys	Asp	Ser	Ser	Tyr

670

agtcgactgc gtcacctgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60
gctgcaccgg gcctggcagc gctccgcaca catttctgt cgcggcctaa gggaaactgt 120
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgtcggg agcgagggcg 180

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<210> 96
<211> 490
<212> PRT
<213> Homo sapiens
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Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly	65	70	75	80
Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu				
				85					90					95					
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly				
			100					105					110						
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu				
		115					120						125						
Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala				
		130				135					140								
Val	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met				
145					150					155					160				
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu				
				165					170					175					
Val	Leu	Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr				
			180					185					190						
Arg	Ala	Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro				
		195					200					205							
Gly	Thr	Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val				
		210				215					220								
Thr	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly				
225					230					235					240				
Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys				
				245					250					255					
Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu				
			260					265					270						
Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr				
		275					280					285							
Ser	Gly	Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg				
		290				295					300								
Arg	Pro	Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro				
305					310					315					320				
Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln				
				325					330					335					
Asp	Asn	Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln				

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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe
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24

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

20

20

24

24

50

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<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
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<400> 103

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 agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgcctt gccggccgcg 120
 tatcccccggt ctacctgggc cgcgccgcgg cgggtgcgcgc gtgagagggg gcgcgcgggc 180
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 ggtgcggagg ggcgtgtgtg ccggcgcgcg cgcctgtggg tgcaaacccc gagcgtctac 300
 gctgccatga ggggcgcgaa cgccgtggcg ccaactctgcc tgetgctggc tgccgccacc 360
 cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
 ggagagtctg gattttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
 tgtacttggg aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
 gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600
 aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
 ggcaacaaga tgatggtgca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
 gccatgttct ccgctgctga accaaacgaa agaggggatc agtattgtgg aggactcctt 780
 gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
 gtcacttgtg tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
 aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
 ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtc accctgcgcca 1020
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 caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
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 gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaaag atgggactgg 1680
 ttgactcttc acatgatgga ggtatgaggg ctccgagata gctgagggaa gttctttgcc 1740
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 ctaaaagtgt caagcgttga cagcttggaa gcgtttatct atacatctct gtaaaaggat 1860
 attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
 gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
 tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
 20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
 35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
 50 55 60

090313 074004
 100720 142050

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

000023 04004
 10020 212000

340

345

350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
 355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
 385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
 405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctogaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

T00120"EF20000

<400> 108

<210> 109

$\langle 211 \rangle$ 420

<212> PRT .

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
50 55 60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
 180 185 190
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

FOOTNOTES

<210> 113

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<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1             5             10             15
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
      20             25             30
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
      35             40             45

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Glu	Glu	Leu	Val	Ile	Pro	Thr	His	Val	Arg	Ala	Gln	Tyr	Val	Ala	Leu
50						55					60				
Leu	Gln	Arg	Ser	His	Gly	Asp	Arg	Ser	Arg	Gly	Lys	Arg	Phe	Ser	Gln
65					70					75					80
Ser	Phe	Arg	Glu	Val	Ala	Gly	Arg	Phe	Leu	Ala	Leu	Glu	Ala	Ser	Thr
				85					90					95	
His	Leu	Leu	Val	Phe	Gly	Met	Glu	Gln	Arg	Leu	Pro	Pro	Asn	Ser	Glu
			100					105					110		
Leu	Val	Gln	Ala	Val	Leu	Arg	Leu	Phe	Gln	Glu	Pro	Val	Pro	Lys	Ala
		115					120					125			
Ala	Leu	His	Arg	His	Gly	Arg	Leu	Ser	Pro	Arg	Ser	Ala	Arg	Ala	Arg
	130					135					140				
Val	Thr	Val	Glu	Trp	Leu	Arg	Val	Arg	Asp	Asp	Gly	Ser	Asn	Arg	Thr
145					150					155					160
Ser	Leu	Ile	Asp	Ser	Arg	Leu	Val	Ser	Val	His	Glu	Ser	Gly	Trp	Lys
				165					170					175	
Ala	Phe	Asp	Val	Thr	Glu	Ala	Val	Asn	Phe	Trp	Gln	Gln	Leu	Ser	Arg
			180					185					190		
Pro	Arg	Gln	Pro	Leu	Leu	Leu	Gln	Val	Ser	Val	Gln	Arg	Glu	His	Leu
		195					200					205			
Gly	Pro	Leu	Ala	Ser	Gly	Ala	His	Lys	Leu	Val	Arg	Phe	Ala	Ser	Gln
	210					215					220				
Gly	Ala	Pro	Ala	Gly	Leu	Gly	Glu	Pro	Gln	Leu	Glu	Leu	His	Thr	Leu
225					230					235					240
Asp	Leu	Gly	Asp	Tyr	Gly	Ala	Gln	Gly	Asp	Cys	Asp	Pro	Glu	Ala	Pro
				245					250					255	
Met	Thr	Glu	Gly	Thr	Arg	Cys	Cys	Arg	Gln	Glu	Met	Tyr	Ile	Asp	Leu
			260					265					270		
Gln	Gly	Met	Lys	Trp	Ala	Glu	Asn	Trp	Val	Leu	Glu	Pro	Pro	Gly	Phe
		275					280					285			
Leu	Ala	Tyr	Glu	Cys	Val	Gly	Thr	Cys	Arg	Gln	Pro	Pro	Glu	Ala	Leu
	290					295					300				
Ala	Phe	Lys	Trp	Pro	Phe	Leu	Gly	Pro	Arg	Gln	Cys	Ile	Ala	Ser	Glu
305					310					315					320
Thr	Asp	Ser	Leu	Pro	Met	Ile	Val	Ser	Ile	Lys	Glu	Gly	Gly	Arg	Thr
				325					330					335	

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 115

aggactgccataacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc	aggagtcctt	cggcggctgt	tgtgtcagtg	gcctgatcgc	gatggggaca	60
aaggcgcaag	tcgagaggaa	actgttgtgc	ctcttcatat	tggcgatcct	gttgtgctcc	120
ctggcattgg	gcagtgttac	agtgcactct	tctgaacctg	aagtcagaat	tcctgagaat	180

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<210> 119
<211> 299
<212> PRT
<213> Homo sapiens
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Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tgatcgcgat qgggacaaaq qcqcaagctc gagaggaaac tgttgtgcct

50

<211> 20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

acacctgggtt caaagatggg

20

<211> 24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

taggaagagt tgctgaaggc acgg

24

<211> 20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

ttgccttact caggtgctac

20

<211> 20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125

actcagcagt ggtaggaaag

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtaccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcca cgccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaagg gatgccaca ccatggggcc ccctgtgacc ctggagagt 600
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agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
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ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc 1210

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala

1

5

10

15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu

20

25

30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly

35

40

45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser

50

55

60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys

65

70

75

80

T00120 E20000

24

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg

24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
 cccacgcgtc cgggtctcgt cgctcgcgca gcggcgccag cagaggtcgc gcacagatgc 60
 ggggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
 gactcttggc cgtgatcctg tggtttcagc tggcgctgtg ctteggccct gcacagctca 300
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
 ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
 gattcaagct gaagggcgt acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
 atgaaggatt caagatccgg taccgccgac tacacaatat ggtttcatta tgcgcgatg 660
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
 atcgctgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
 ctccaatggt gagtcacgga gatttcgtct gccaccgcg gccttgtag cgctacaacc 960
 acggaactgt ggtggagttt tactgcgac ctggctacag cctcaccagc gactacaagt 1020
 acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaactcag 1080
 agcaaactg gccccagcacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140

cggcaaccag tgtgtgtgtg gtgtgtgtgc tegtcatcct ggccaggatg ttccagacca 1200
 agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
 ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
 gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccgc 1380
 tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
 ctcccagggtg ccaagagagc acccacccctg cttcggacaa ccctgacata attgccagca 1560
 cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttgttcc 1620
 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
 ctgatacctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

000033034004

180							185					190				
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
195							200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
210							215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225							230					235				
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
245							250					255				
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
260							265					270				
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	
275							280					285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys	
290							295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr	
305							310					315				
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu	
325							330					335				
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His	
340							345					350				
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe	
355							360					365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala	
370							375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val	
385							390					395				
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr	
405							410					415				
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys	
420							425					430				
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro	
435							440					445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile	
450							455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctcccgctg cggtcgcgtc gtggcctaga 60
gatgctgctg ccgcgggttg agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120
ccgtagcggc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tgggctgctg ggccgcgacg ggtcgctgct 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tectgcgga 600
 gcgaggtctg cgtggtcag taccatcagc catcggcacc cgctggcacc ggaggccct 660
 acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
 ctgatgagaa accagcagtt cttctagag aagctgaagg tgaggaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccctt ctctctctcc 900
 ttgtggtcac cacagttgta tgttgggtt ggatctgtag aaaaagaaaa cgggagcagc 960
 cagaccctag cacaagaag caacacacca tctggccctc tctcaccag ggaaacagcc 1020
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
 tgtcttgatga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccc gaccaaattg 1260
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
 aaactgaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta tttctataa 1380
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tctgtggat gagcatgtgg 1440
 tccccacgac ctctgtttg acccccacgt tttggtgta tctttatcc cagccagtca 1500
 tccagctcga cttatgaga aggtacctg ccaggtctg gcacatagta gagtctcaat 1560
 aaatgtcact tggttggtt tatctaact ttaagggaca gagctttacc tggcagtgat 1620
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat ctttcaaag cccacatatg gtagcacagg 1740
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaataaag 1800
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
 100 105 110

<210> 138

<400>	141						
gggggtctccc	tcaggggccgg	gagggcacagc	ggtccctgct	tgctgaaggg	ctggatgtac	60	
gcatccgcag	gttcccgcg	acttggggggc	gcccgctgag	ccccggcgcc	cgcagaagac	120	
ttgtgtttgc	ctcctgcagc	ctcaaccgcg	agggcagcga	gggcctacca	ccatgatcac	180	
tgggtgtgttc	agcatgcgct	tgtggacccc	agtgggcgtc	ctgacctcgc	tggcgtactg	240	
cctgcaccag	cggcgggtgg	ccctggccga	gctgcaggag	gccgatggcc	agtgtccggg	300	
cgaccgcagc	ctgctgaagt	tgaaaatggt	gcaggtcgtg	tttcgacacg	gggctcggag	360	
tcctctcaag	ccgctccgc	tggaggagca	ggtagagtgg	aacccccagc	tattagaggt	420	
ccccacccaa	actcagtttg	attacacagt	caccaatcta	gctggtggtc	cgaaaccata	480	
ttctccttac	gactctcaat	accatgagac	caccttgaag	gggggcatgt	tgtctgggca	540	
gctgaccaag	gtgggcatac	agcaaatggt	tgccttggga	gagagactga	ggaagaacta	600	
tgtggaagac	attccctttc	tttcaccaac	cttcaaccca	caggaggtct	ttattcgttc	660	
cactaacatt	tttcggaatc	tggagtccac	ccgttgtttg	ctggctgggc	ttttccagtg	720	

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgctc 840
 ttacagcca ggaatctcag aggatttgaa aaaggtgaag gacaggatgg gcattgacag 900
 tagtgataaa gtggacttct tcatcctcct ggacaacgtg gctgccgagc aggcacacaa 960
 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
 cacatccttg tacatactgc ccaaggaaga cagggaagt cttcagatgg cagtaggcc 1080
 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200
 gaccctgggg atttttgacc acaaatggcc accgtttgct gttgacctga ccatggaact 1260
 ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
 ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
 agtttatacc ttaagccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
 agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
 gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1 5 10 15
 Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30
 Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45
 Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60
 Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80
 Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95
 Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110
 Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125
 Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130 135 140
 Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145 150 155 160
 Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
 165 170 175

00004-0004

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<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa cataacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

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<210> 148
<211> 347
<212> PRT
<213> Homo sapiens
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Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

```
<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg	gttctatcga	ttgaattccc	cggggatcct	ctagagatcc	ctcgacctcg	60
acccacgcgt	ccgcggacgc	gtgggcggac	gcgtgggccc	gctaccagga	agagtctgcc	120
gaaggtgaag	gccatggact	tcatcacctc	cacagccatc	ctgcccctgc	tggtcggctg	180
cctgggcgct	ttcgccctct	tccggctgct	gcagtgggtg	cgcggaagg	cctacctgcg	240
gaatgctgtg	gtggtgatca	caggcgccac	ctcagggtg	ggcaaagaat	gtgcaaaagt	300
cttctatgct	gcgggtgcta	aactggtgct	ctgtggccgg	aatggtgggg	ccctagaaga	360
gctcatcaga	gaacttaccg	cttctcatgc	caccaagggtg	cagacacaca	agccttactt	420
ggtgaccttc	gacctcacag	actctggggc	catagttgca	gcagcagctg	agatcctgca	480
gtgctttggc	tatgtcgaca	tacttgtcaa	caatgctggg	atcagctacc	gtggtaccat	540
catggacacc	acagtggatg	tggacaagag	ggtcatggag	acaaactact	ttggcccagt	600
tgtctaaacg	aaagcactcc	tgccctccat	gatcaagagg	aggcaaggcc	acattgtcgc	660
catcagcagc	atccagggca	agatgagcat	tccttttcga	tcagcatatg	cagcctccaa	720
gcacgcaacc	caggctttct	ttgactgtct	gcgtgccgag	atggaacagt	atgaaattga	780
ggtgaccgtc	atcagccccg	gctacatcca	caccaacctc	tctgtaaatg	ccatcaccgc	840
ggatggatct	aggtatggag	ttatggacac	caccacagcc	cagggccgaa	gccctgtgga	900
ggtggccccg	gatgttcttg	ctgctgtggg	gaagaagaag	aaagatgtga	tcctggctga	960
cttactgcct	tccttggtctg	tttatcttcg	aactctggct	cctgggctct	tcttcagcct	1020
catggcctcc	agggccagaa	aagagcggaa	atccaagaac	tcctagtact	ctgaccagcc	1080

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<210> 153
<211> 310
<212> PRT
<213> Homo sapiens
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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

220

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 156
tcatactgtt ccatctcggc acgc

24

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157
aatgggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacacccaaa cgctcgcagc caaaaagggt atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggaactgg gtgccaaagg 360
tcataacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaagg 420
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggtgtag tctatacatc 480
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tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaacaa catgtctgtg tctaatttc gtaaacactg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactct ggaacctgag gaagtggtaa acaggctgat 840
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cttctgtttt ttctaattat cccattttct tcaatatcat ttttgaggct ttggcagtct 1140
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gccactctgt ttcttgagag atacctcaca ttccaatgcc aaacatttct gcacagggaa 1560
gctagagggtg gatacacgtg ttgcaagtat aaaagcatca ctgggattta aggagaattg 1620
agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

<212> PRT

<213> Homo sapiens

<400> 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
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20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
130 135 140

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255

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 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240
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 caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
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 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggtttga ggcccttgaa 960
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 gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaat ggatgaagct 1980
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 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65				70				75				80			
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

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<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

50

<213> Homo sapiens

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tcttgctgga	gaagaaaggg	ctgagggcag	agcagggcac	tctcactcag	ggtgaccagc	180
tccttgcttc	tctgtggata	acagagcatg	agaaagtga	gagatgcagc	ggagtgaggt	240
gatggaagtc	taaaatagga	aggaatTTTg	tgtgcaatat	cagactctgg	gagcagttga	300
cctggagagc	ctggggggagg	gcctgcctaa	caagctttca	aaaaacagga	gcgacttcca	360
ctgggctggg	ataagacgtg	ccggtaggat	aggggaagact	gggttttagtc	ctaatatcaa	420
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cttaaggggc	cagaaataga	gatgctttgt	aaaataaaaat	tttaaaaaaa	gcaagtattt	540
tatagcataa	aggctagaga	ccaaaataga	taacaggatt	ccctgaacat	tcctaagagag	600
gagaaagtat	gttaaaaaata	gaaaaccacaa	aatgcagaag	gaggagactc	acagagctaa	660
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tctgaccact	ctgccttgtg	ttttgcagaa	tcatgtgagg	gccaaaccggg	gaaggtggag	780
cagatgagca	cacacaggag	ccgtctcctc	accgccgcc	ctctcagcat	ggaacagagg	840
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aatcgtgact	ggaccttcaa	ccacttgacc	gtccaccaag	ggacgggggc	cgtctatgtg	1020
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gaagtgtcca	ccctcaccaa	caatgtcaac	aagctgctca	tcattgacta	ctctgagaac	1200
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ctcatcaaga	tcctctcaga	cagcctggcc	ctggctccc	actttgacat	cttctacatc	1560
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ggtgtggcca	tcaactccgc	tggagacctc	ttctacacct	cacgcacgt	gcggctctgc	1680

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<210> 170
<211> 552
<212> PRT
<213> Homo sapiens
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<400> 170																
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			20					25					30			
Gln	Pro	Gly	Lys	Val	Glu	Gln	Met	Ser	Thr	His	Arg	Ser	Arg	Leu	Leu	
		35					40					45				
Thr	Ala	Ala	Pro	Leu	Ser	Met	Glu	Gln	Arg	Gln	Pro	Trp	Pro	Arg	Ala	
	50					55					60					
Leu	Glu	Val	Asp	Ser	Arg	Ser	Val	Val	Leu	Leu	Ser	Val	Val	Trp	Val	
65					70					75					80	
Leu	Leu	Ala	Pro	Pro	Ala	Ala	Gly	Met	Pro	Gln	Phe	Ser	Thr	Phe	His	
				85					90					95		
Ser	Glu	Asn	Arg	Asp	Trp	Thr	Phe	Asn	His	Leu	Thr	Val	His	Gln	Gly	
			100					105					110			
Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr	
		115					120					125				
Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp	
	130					135					140					
Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val	
145					150					155					160	
Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser	
				165					170					175		

Glu	Asn	Arg	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Tyr	Gln	Gly	Val	Cys	Lys	
			180				185						190			
Leu	Leu	Arg	Leu	Asp	Asp	Leu	Phe	Ile	Leu	Val	Glu	Pro	Ser	His	Lys	
			195				200				205					
Lys	Glu	His	Tyr	Leu	Ser	Ser	Val	Asn	Lys	Thr	Gly	Thr	Met	Tyr	Gly	
			210				215						220			
Val	Ile	Val	Arg	Ser	Glu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Gly	Thr	
225						230				235			240			
Ala	Val	Asp	Gly	Lys	Gln	Asp	Tyr	Phe	Pro	Thr	Leu	Ser	Ser	Arg	Lys	
			245						250			255				
Leu	Pro	Arg	Asp	Pro	Glu	Ser	Ser	Ala	Met	Leu	Asp	Tyr	Glu	Leu	His	
			260						265			270				
Ser	Asp	Phe	Val	Ser	Ser	Leu	Ile	Lys	Ile	Pro	Ser	Asp	Thr	Leu	Ala	
			275						280			285				
Leu	Val	Ser	His	Phe	Asp	Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly	
			290			295						300				
Gly	Phe	Val	Tyr	Phe	Leu	Thr	Val	Gln	Pro	Glu	Thr	Pro	Glu	Gly	Val	
305						310						315			320	
Ala	Ile	Asn	Ser	Ala	Gly	Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg	
			325						330			335				
Leu	Cys	Lys	Asp	Asp	Pro	Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe	
			340						345			350				
Gly	Cys	Thr	Arg	Ala	Gly	Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr	
			355						360			365				
Leu	Ala	Lys	Pro	Gly	Asp	Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser	
			370			375						380				
Gln	Asp	Asp	Val	Leu	Phe	Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr	
385						390						395			400	
His	His	Pro	Pro	Asp	Asp	Ser	Ala	Leu	Cys	Ala	Phe	Pro	Ile	Arg	Ala	
			405						410			415				
Ile	Asn	Leu	Gln	Ile	Lys	Glu	Arg	Leu	Gln	Ser	Cys	Tyr	Gln	Gly	Glu	
			420						425			430				
Gly	Asn	Leu	Glu	Leu	Asn	Trp	Leu	Leu	Gly	Lys	Asp	Val	Gln	Cys	Thr	
			435						440			445				
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<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe
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<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc 24

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<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

42

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<221> modified_base
<222> (1683)
<223> a, t, c or g
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tgctggtcgt	cttgggcttc	ctggtgctcc	gcaggctgga	ctggagcacc	ctggctccctc	180	
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cgggtggacc	ccctcctgct	ggtgccagt	ggagactgcc	gcctcctctt	gacctgaagc	2040	
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<210> 175
<211> 636
<212> PRT
<213> Homo sapiens
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<220>
<221> MOD_RES
<222> (539)
<223> Any amino acid
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<400> 175
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20                      25                  30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35                     40                   45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
    50                          55                 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
   65                        70               75             80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85                             90                    95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100                           105                110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
     115                            120                125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
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Leu 145	Gly	Gly	Leu	Pro	Ser 150	Trp	Leu	Leu	Gln	Asp 155	Pro	Gly	Met	Arg	Leu 160
Arg	Thr	Thr	Tyr	Lys 165	Gly	Phe	Thr	Glu	Ala 170	Val	Asp	Leu	Tyr	Phe 175	Asp
His	Leu	Met	Ser 180	Arg	Val	Val	Pro	Leu 185	Gln	Tyr	Lys	Arg	Gly 190	Gly	Pro
Ile	Ile	Ala 195	Val	Gln	Val	Glu	Asn 200	Glu	Tyr	Gly	Ser	Tyr 205	Asn	Lys	Asp
Pro	Ala 210	Tyr	Met	Pro	Tyr	Val 215	Lys	Lys	Ala	Leu	Glu 220	Asp	Arg	Gly	Ile
Val 225	Glu	Leu	Leu	Leu	Thr 230	Ser	Asp	Asn	Lys	Asp 235	Gly	Leu	Ser	Lys	Gly 240
Ile	Val	Gln	Gly	Val 245	Leu	Ala	Thr	Ile	Asn 250	Leu	Gln	Ser	Thr	His 255	Glu
Leu	Gln	Leu	Leu 260	Thr	Thr	Phe	Leu	Phe 265	Asn	Val	Gln	Gly	Thr 270	Gln	Pro
Lys	Met 275	Val	Met	Glu	Tyr	Trp	Thr 280	Gly	Trp	Phe	Asp 285	Ser	Trp	Gly	Gly
Pro 290	His	Asn	Ile	Leu	Asp	Ser 295	Ser	Glu	Val	Leu	Lys 300	Thr	Val	Ser	Ala
Ile 305	Val	Asp	Ala	Gly	Ser 310	Ser	Ile	Asn	Leu	Tyr 315	Met	Phe	His	Gly	Gly 320
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Ser	Asp	Val	Thr 340	Ser	Tyr	Asp	Tyr	Asp 345	Ala	Val	Leu	Thr	Glu 350	Ala	Gly
Asp	Tyr 355	Thr	Ala	Lys	Tyr	Met	Lys 360	Leu	Arg	Asp	Phe	Phe 365	Gly	Ser	Ile
Ser 370	Gly	Ile	Pro	Leu	Pro	Pro 375	Pro	Pro	Asp	Leu	Leu 380	Pro	Lys	Met	Pro
Tyr 385	Glu	Pro	Leu	Thr	Pro 390	Val	Leu	Tyr	Leu	Ser 395	Leu	Trp	Asp	Ala	Leu 400
Lys	Tyr	Leu	Gly	Glu 405	Pro	Ile	Lys	Ser	Glu 410	Lys	Pro	Ile	Asn	Met 415	Glu
Asn	Leu	Pro	Val 420	Asn	Gly	Gly	Asn 425	Gly	Gln	Ser	Phe	Gly	Tyr 430	Ile	Leu

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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1             5             10             15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
      20             25             30

```

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Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35             40             45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50             55             60

```

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				85					90					95	
Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala
			100					105					110		
Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp
		115					120					125			
Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His
	130					135					140				
Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe
145					150					155					160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly
				165					170					175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala
			180					185					190		
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu
		195					200					205			
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu
	210					215					220				
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro
225					230					235					240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro
				245					250					255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr
			260					265					270		
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly
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Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe
	290					295					300				
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly
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Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser
				325					330					335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile

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Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro						
		355					360					365									
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu						
	370					375					380										
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu						
385					390					395					400						
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr						
				405					410					415							
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val						
			420					425					430								
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val						
	435						440					445									
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr						
	450					455					460										
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg						
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Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro						
				485					490					495							
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu						
			500					505					510								
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys						
		515					520					525									
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr						
	530					535					540										
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly						
545					550					555					560						
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr						
				565					570					575							
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu						
			580					585					590								
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu						
		595					600					605									
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu						
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe.

<400> 180

gggcttcacc gaagcagtgg acctttattt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 181

ccaqctatga ctatgatgca cc

22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcaccag aatggtgtg gctc

24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
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 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tocaagcggt 300
 ttggtgtgtt cttgtcagaa gttagtga aaacttag ggaaattagt ttgaacctag 360
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420
 tgcactgtgt catgctgtcg ggggtgccc atgctgtctt tgacctcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
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 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
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 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080
 aaattgttac tattctctcc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaa ctcagatgct 1200
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
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<210> 185
<211> 501
<212> PRT
<213> Homo sapiens
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<400> 185															
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Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
			20					25					30		
Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
		35					40					45			
Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
	50					55					60				
Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
65					70					75					80
Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
				85					90					95	
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
			100					105					110		
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
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Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
	130					135					140				
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
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Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
				165					170					175	
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
			180					185					190		

Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu		
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Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu		
210						215						220					
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser		
225						230						235				240	
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu		
245						250						255					
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn		
260						265						270					
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys		
275						280						285					
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln		
290						295						300					
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile		
305						310						315				320	
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn		
325						330						335					
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu		
340						345						350					
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val		
355						360						365					
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile		
370						375						380					
Ser	Met	Ile	Pro	Ile	Glu	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	His	Leu		
385						390						395				400	
His	Ile	Thr	Gly	Asn	Lys	Val	Asp	Ile	Leu	Pro	Lys	Gln	Leu	Phe	Lys		
405						410						415					
Cys	Ile	Lys	Leu	Arg	Thr	Leu	Asn	Leu	Gly	Gln	Asn	Cys	Ile	Thr	Ser		
420						425						430					
Leu	Pro	Glu	Lys	Val	Gly	Gln	Leu	Ser	Gln	Leu	Thr	Gln	Leu	Glu	Leu		
435						440						445					
Lys	Gly	Asn	Cys	Leu	Asp	Arg	Leu	Pro	Ala	Gln	Leu	Gly	Gln	Cys	Arg		
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aaqacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tctctccctg 180
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acattggcat tgetttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
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 atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
 ttcaaaatcac acaacgcgct aaaagctgca aaggaaacctg aagctgtggc tgtaaaaaat 420
 cacaacccag acaagggtgtg gtggggccaag aacagccagg ccaaaaccat tgccacggag 480
 tcttgtcctg ccttgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
 ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ccttctcaa 600
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660
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 cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagtt 780
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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu
	50					55					60			Arg
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu
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Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly
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Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp
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145					150					155				160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro
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Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys
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Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys
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Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile
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Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val
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Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val
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Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp
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Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe
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Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu
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Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys
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Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys
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Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg
	530					535					540				
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu
545					550					555					560
Thr	Pro	Asn	Gln	Pro	Phe	Asn	Ser	Val	His	Leu	Phe	Ser	Phe	Met	Val

575

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oligonucleotide probe

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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<211> 2362
<212> DNA
<213> Homo sapiens
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 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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1

5

10

15

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20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe
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Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro
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Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe
			100					105					110		
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Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp
145					150					155					160
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg
				165					170					175	
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu
		180						185					190		
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
		195					200					205			
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val
	210					215					220				
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225					230					235					240
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr
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His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr
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Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val
305					310					315					320
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<213> Artificial sequence
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<400> 201

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<212> DNA
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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22

<211> 24

<212> DNA

<213> Artificial Sequence.

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggagcagga ggagtagtag tagg

24

<211> 50

<212> DNA

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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50

<211> 1620

<212> DNA

<213> Homo sapiens

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<223> a, t, c or g

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<223> a, t, c or g

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acatactccc cacaccaggt tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20

25

30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35

40

45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50

55

60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65

70

75

80

24

ggacagctcg	cggccccga	gagctctagc	cgtcgaggag	ctgcctgggg	acgtttgccc	60
tggggcccca	gcctggcccg	ggtcacccgtg	gcattgaggag	atgggcctgt	tgctcctggg	120
cccattgtct	ctgctgcccg	gctcctacgg	actgcccttc	tacaacggct	tctactactc	180
caacagcgcc	aacgaccaga	acctaggcaa	cggtcattggc	aaagacctcc	ttaatggagt	240
gaagctggtg	gtggagacac	ccgaggagac	cctgttcacc	taccaagggg	ccagtgtgat	300
cctgccctgc	cgctaccgct	acgagccggc	cctggctctcc	ccgcggcgtg	tgcgtgtcaa	360
atggtggaag	ctgtcggaga	acggggcccc	agagaaggac	gtgctggtgg	ccatcgggct	420
gaggcaccgc	tcctttgggg	actaccaagg	ccgcgtgcac	ctgcggcagg	acaaagagca	480
tgacgtctcg	ctggagatcc	aggatctgcg	gctggaggac	tatgggcgtt	accgctgtga	540
ggtcattgac	gggctggagg	atgaaagcgg	tctgggtggag	ctggagctgc	ggggtgtggg	600

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<210> 213
<211> 360
<212> PRT
<213> Homo sapiens
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<400> 213
Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
      20                      25                      30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
      35                      40                      45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
  50                      55                      60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
  65                      70                      75                      80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
      85                      90                      95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
      100                      105                      110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130 135 140		
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145 150 155 160		
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165 170 175		
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180 185 190		
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195 200 205		
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210 215 220		
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225 230 235 240		
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245 250 255		
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260 265 270		
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275 280 285		
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290 295 300		
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305 310 315 320		
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325 330 335		
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340 345 350		
Gly Val Tyr Cys Tyr Arg Gln His 355 360		

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

18

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<210> 219

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag

45

<210> 220

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 220

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tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcccc 180
cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
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cgcgggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360
gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
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tgcttggcct ggcttgggac acctcctctc tgccaggagg caataaaagc cagcgccggg 1440
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aaa 1503

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<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

1000-1-100000

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 225

ccccctgag cgacgctccc ccatgatgac gccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens.

<400> 226

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ggggccttgc cttccgcact cgggcccagc cgggtggatc tcgagcaggt ggggagcccc 60
ggggcggcggg cgcgggtgag agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
ccagcctgtc tgtcgtcggt ttggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180
atcctgggct tcgctcgatt tgccgcagag gcgcctccca gacctagagg ggcgctggcc 240
tggagcagcg ggtcgtctgt gtccctctct ctctgcgcgc cggccgggga tccgaagggt 300
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tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gaggttcacag 1980
gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
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attgtattct cataatactg aaatgcttta gcatactaga atcagataga aaactattaa 2160
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aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gcctactaaa 2340
tgtacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaa 2400
aaa
2403

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<210> 227

<400> 227

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255

Phe Leu Glu Ser Gln Gln
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

FOOTNOTES

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttctcaaga gggcagcc

18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc

24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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 ccggcggcct ccggcgggga gcgagcagat ccagtcgggc ccgcagcgca actcgggtcca 120
 gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180
 gcctgctgct ggcggcgccg gtccccacgg ccccgcgcc cgctccgacg gcgacctcgg 240
 ctccagtcaa gcccggcccc gctctcagct acccgagga ggaggccacc ctcaatgaga 300
 tggtccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480
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 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcatcatcg 600
 acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

<210> 237

<211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 ggagctgcac cccttgc

17

<210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 238
 ggaggactgt gccacatga gagactcttc aaaccaagg caaaattgg

49

<210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 239
 gcagagcgga gatgcagcgg cttg

24

<210> 240
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 240
 ttggcagctt catggagg

18

<210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 241
 cctgggcaaa aatgcaac

18

100420230600

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgcacct cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg

45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 cacacataca ccttcctctc cttcactgaa gactcacagt cactcactct 200
 gtgagcaggt catagaaaag gacactaaag cottaaggac aggcttgccc 250
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 gaatccagga ggcggaggat gcagtcagct gagggcaccg ctgcactcca 550
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 ccaacctcct gagggccatt gacagccgt ggtttgaaat gctgccaac 1450
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 ccttcatcca ccccgcgcc ttccaccacc tgccccagat ggagaccctc 1900
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagt 1950

THE **NEW** **YORK** **PUBLIC** **LIBRARY**

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<210> 245
<211> 713
<212> PRT
<213> Homo Sapien
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				20					25					30
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
				35					40					45
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
				50					55					60
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
				65					70					75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
				80					85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
				95					100					105
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
				125					130					135
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
				140					145					150

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser
				155					160					165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile
				170					175					180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met
				185					190					195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg
				200					205					210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu
				215					220					225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu
				230					235					240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg
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Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys
				260					265					270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu
				275					280					285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser
				290					295					300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu
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Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn
				335					340					345
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				350					355					360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys
				365					370					375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile
				380					385					390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg
				395					400					405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys

				410					415					420
Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435
Ala	Ser	Gly	Glu	Ser 440	Met	Val	Leu	His	Cys 445	Arg	Ala	Leu	Ala	Glu 450
Pro	Glu	Pro	Glu	Ile 455	Tyr	Trp	Val	Thr	Pro 460	Ala	Gly	Leu	Arg	Leu 465
Thr	Pro	Ala	His	Ala 470	Gly	Arg	Arg	Tyr	Arg 475	Val	Tyr	Pro	Glu	Gly 480
Thr	Leu	Glu	Leu	Arg 485	Arg	Val	Thr	Ala	Glu 490	Glu	Ala	Gly	Leu	Tyr 495
Thr	Cys	Val	Ala	Gln 500	Asn	Leu	Val	Gly	Ala 505	Asp	Thr	Lys	Thr	Val 510
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Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
Leu	Ile	Ala	Ile	Leu 635	Ala	Leu	Ala	Val	Leu 640	Leu	Leu	Ala	Ala	Gly 645
Leu	Ala	Ala	His	Leu 650	Gly	Thr	Gly	Gln	Pro 655	Arg	Lys	Gly	Val	Gly 660
Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675

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<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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				20					25					30

Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40					45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55					60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70					75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85					90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

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95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu	Ile Asp Gln Tyr Asp Pro	
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe	Leu Ser Glu Val Ser Glu	
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu Asp	
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu Glu	
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile	Pro Asp Thr Val Phe Asp	
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp Val	
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu Leu	
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu Ala	
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu	His Ile Lys Phe Thr Asp	
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu Glu	
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg Tyr	
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val Leu	
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu	Pro Gln Val Val Thr Asp	
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly Thr	
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu Thr	
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu	Glu Arg Ile Pro His Ser	
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu	Ile Asp Leu Lys Asp Asn	
350	355	360

F00T20" E F 20660

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
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Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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Ala	Asp	Lys	Glu	Gln	Ala									
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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

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<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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<211> 452

<212> PRT

<213> Homo Sapien

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				20					25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
				35					40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
				50					55					60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
				65					70					75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
				80					85					90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
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				110					115					120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
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Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
				140					145					150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser
				155					160					165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
				170					175					180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
				185					190					195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
				200					205					210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
				215					220					225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
				230					235					240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys
				245					250					255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr
				260					265					270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser
				275					280					285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His
				290					295					300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

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Gly Gly Gln Ala	Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe
335	340	345
Met Lys Pro Val	Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly
350	355	360
Ile Asn Val Thr	Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp
365	370	375
Thr Met Gly Gln	Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu
380	385	390
Leu Pro Lys Phe	Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp
395	400	405
Pro Lys Ser Leu	Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn
410	415	420
Leu Ala Phe Tyr	Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser
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Asp Gln Gly Asp	Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
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<400> 257
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
  1          5          10          15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
          20          25          30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
          35          40          45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
          50          55          60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
          65          70          75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
          80          85          90

```

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

P00100 "E22000"

ctccttaggg	ctcttttgccc	tcacccctctc	tggcaaatgc	agttacagcc	100
cggagcccga	ccagcggagg	acgctgcccc	caggctgggt	gtccctgggc	150
ctg'gcggacc	ctgaggaaga	gctgagtctc	acctttgccc	tgagacagca	200
gaatgtggaa	agactctcgg	agctgggtgca	ggctgtgtcg	gatcccagct	250
ctcctcaata	cggaaaatac	ctgaccctag	agaatgtggc	tgatctggtg	300
aggccatccc	cactgaccct	ccacacgggtg	caaaaatggc	tcttggcagc	350
cggagcccag	aagtgccatt	ctgtgatcac	acaggacttt	ctgacttgct	400
ggctgagcat	ccgacaagca	gagctgctgc	tccctggggc	tgagtttcat	450
cactatgtgg	gaggacctac	ggaaacccat	gttgtaagg	ccccacatcc	500
ctaccagctt	ccacaggcct	tggcccccca	tgtggacttt	gtggggggac	550
tgcaccgttt	tcccccaaca	tcacccctga	ggcaacgtcc	tgagccgcag	600
gtgacaggg	ctgtaggcct	gcacctgggg	gtaaccccct	ctgtgatccg	650
taagcgatac	aacttgacct	cacaagacgt	gggctctggc	accagcaata	700
acagccaagc	ctgtgcccag	ttcctggagc	agtatttcca	tgactcagac	750
ctggctcagt	tcacgcgcct	cttcgggtggc	aactttgcac	atcaggcatc	800
agtagcccg	gtggttgag	aacagggccg	gggccggg	gggattgagg	850
ccagtctaga	tgtgcagtac	ctgatgagt	ctggtgccaa	catctccacc	900
tgggtctaca	gtagccctgg	ccggcatgag	ggacaggagc	ccttctctga	950
gtgggtcatg	ctgctcagta	atgagtcagc	cctgccacat	gtgcatactg	1000
tgagctatgg	agatgatgag	gactccctca	gcagcgcta	catccagcgg	1050
gtcaacactg	agctcatgaa	ggctgccgct	cggggctctca	ccctgctctt	1100
cgccctcagg	gacagtgggg	ccgggtgttg	gtctgtctct	ggaagacacc	1150
agttccgccc	taccttcct	gcctccagcc	cctatgtcac	cacagtggga	1200
ggcacatcct	tccaggaacc	tttctctatc	acaaatgaaa	ttgttgacta	1250
tatcagtggt	ggtggcttca	gcaatgtgtt	cccacggcct	tcataccagg	1300
aggaagctgt	aacgaagttc	ctgagctcta	gccccacct	gccaccatcc	1350
agttacttca	atgccagtgg	ccgtgcctac	ccagatgtgg	ctgcactttc	1400

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<210> 259
<211> 556
<212> PRT
<213> Homo Sapien
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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20										25				30			
Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu			
				35					40					45			
Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg			
				50					55					60			
Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln			
				65					70					75			
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg			
				80					85					90			
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala			
				95					100					105			
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu			
				110					115					120			
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly			
				125					130					135			
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val			
				140					145					150			
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro			
				155					160					165			
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser			
				170					175					180			
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly			
				185					190					195			
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn			
				200					205					210			
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln			
				215					220					225			
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu			
				230					235					240			
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala			
				245					250					255			
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly			
				260					265					270			
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala			
				275					280					285			

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly	290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser	305	310	315
Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp	320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met	335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp	350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg	365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly	380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp	395	400	405
Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser	410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His	425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro	440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg	455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val	470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser	485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln	500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser	515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro	530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu	545	550	555

F00720"ET230600

```
<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien
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<400> 260
gccgcgcgcgt ctctcccgcc gccacacact gtctgagcgg cgcagcgagc 50
cgcgcccccgg gcgggctgct cggcgcggaa cagtgtctcg catggcaggg 100
attccagggc tcctcttcct tctcttcttt ctgctctgtg ctgttgggca 150
agtgagccct tacagtgcct cctggaaacc cacttggcct gcataccgcc 200
tcctgtcgt cttgccccag tctacctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac ccagtgctca 300
taagggaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actaccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcttaaagc ccaagtttaa agatggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttg atcaagggca 800
atgccaatga catcggcag gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctctgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggg 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100
```

```
<210> 261
<211> 383
<212> PRT
<213> Homo Sapien
```

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	
1				5					10					15	
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	
				20					25					30	
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	
				35					40					45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	
				50					55					60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	
				65					70					75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	
				80					85					90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	
				95					100					105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	
				110					115					120	

[illegible]

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
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 ccatgggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100
 accttcacct cctgctgct gctggcgctg acagccatcc tcaatgcggc 150
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
 ttgtggggcg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccca ccaactgcgc ggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
 cgggtccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctgagcgct 500
 ccatacagtt ctgagagcgg gtccctgccca tctgcctacc tgatgcctct 550
 atccacctcc ctccaaacac ccaactgctg atctcaggtt gggggagcat 600
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttgagggg 750
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
 gccgagcgca acaggcccg ggtctacatc agcctctctg cgcaccgctc 900
 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgcgta 1100
 aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctccccgacc cgcccgacgg cctcaggccc cctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttcggc 1250
 cccgcccccg ggccccagcg cttttgtgta tataaatggt aatgattttt 1300
 ataggtattt gtaacctgc ccacatatct tattttattcc tccaatttca 1350
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly Ser Ile Gln Asp Gly Val Pro Leu	Pro His Pro Gln Thr Leu
185	190 195
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His	
200	205 210
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met	
215	220 225
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly	
230	235 240
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu	
245	250 255
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn	
260	265 270
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val	
275	280 285
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly	
290	295 300
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala	
305	310 315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

agctctagac caatgccagc ttcc 24

<211> 45

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<211> 25

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

ggggaattca ccctatgaca ttgcc 25

<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gaatgccctg caagcatcaa ctgg 24

<211> 50

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc cccgac 45

<210> 276

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 276

gggcagggat tccagggctc c 21

<210> 277

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 277

ggctatgaca gcaggttc 18

<210> 278

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 278

tgacaatgac cgaccagg 18

<210> 279

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 279

gcacgcatt gctggttagag caag 24

<210> 280

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgtg 50

ccgtactgc tactgtgtgt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag	aaacgtttga	tggtggagct	gcacaacctc	taccggggccc	150
aggtatcccc	gacggcctca	gacatgctgc	acatgagatg	ggacgaggag	200
ctggccgcct	tgcceaaggc	ctacgcacgg	cagtgcgtgt	ggggccacaa	250
caaggagcgc	gggcgccgcg	gcgagaatct	gttcgccatc	acagacgagg	300
gcatggacgt	gccgctggcc	atggaggagt	ggcaccacga	gcgtgagcac	350
tacaacctca	gcgccgccac	ctgcagccca	ggccagatgt	gcggccacta	400
cacgcagggt	gtatgggcca	agacagagag	gatcggctgt	ggttcccact	450
tctgtgagaa	gctccaggg	gttgaggaga	ccaacatcga	attactgggt	500
tgcaactatg	agcctccggg	gaacgtgaag	gggaaacggc	cctaccagga	550
ggggactccg	tgctcccaat	gtccctctgg	ctaccactgc	aagaactccc	600
tctgtgaacc	catcggaagc	ccggaagatg	ctcaggattt	gccttacctg	650
gtaactgagg	ccccatcctt	ccgggcgact	gaagcatcag	actctaggaa	700
aatgggtact	ccttcttccc	tagcaacggg	gattccggct	ttcttggtaa	750
cagagggtctc	aggctccctg	gcaaccaagg	ctctgcctgc	tgtggaaacc	800
caggccccaa	cttccttagc	aacgaaagac	ccgccctcca	tggcaacaga	850
ggctccacct	tgcgtaacaa	ctgagggtccc	ttccattttg	gcagctcaca	900
gcctgccctc	cttggatgag	gagccagtta	ccttccccaa	atcgacccat	950
gttcctatcc	caaaatcagc	agacaaagtg	acagacaaaa	caaaagtgcc	1000
ctctaggagc	ccagagaact	ctctggaccc	caagatgtcc	ctgacagggg	1050
caagggaact	cctaccccat	gcccaggagg	aggctgaggc	tgaggctgag	1100
ttgcctcctt	ccagtgaggt	cttggcctca	gtttttccag	cccaggacaa	1150
gccagggtgag	ctgcaggcca	cactggacca	cacggggcac	acctcctcca	1200
agtccttgcc	caatttcccc	aatacctctg	ccaccgctaa	tgccacgggt	1250
gggcgtgccc	tggctctgca	gtcgtccttg	ccaggtgcag	agggccctga	1300
caagcctagc	gttgtgtcag	ggctgaactc	gggccctgg	catgtgtggg	1350
gccctctcct	gggactactg	ctcctgcctc	ctctgggtgtt	ggctggaatc	1400

ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
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 Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180
 Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195
 Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
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 Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225
 Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240
 Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255
 Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270
 Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285
 Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300
 Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315
 Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330
 Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345
 Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360
 Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375
 Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390
 Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

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<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

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<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic Oligonucleotide Probe

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<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien
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<400> 289
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ctttttcaca	ttagcagacc	ggacttaagt	cacaacagat	tatctttcat	150
caaggcaagt	tccatgagcc	accttcaaag	ccttcgagaa	gtgaaactga	200
acaacaatga	attggagacc	attccaaatc	tgggaccagt	ctcggcaaat	250
attacacttc	tctccttggc	tggaaacagg	attgttgaaa	tactccctga	300
acatctgaaa	gagtttcagt	cccttgaaac	tttggacctt	agcagcaaca	350
atatttcaga	gctccaaact	gcatttccag	ccctacagct	caaatatctg	400
tatctcaaca	gcaaccgagt	cacatcaatg	gaacctgggt	attttgacaa	450
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aaccgaaaca	agattaaaaa	tgtagatgga	ctgacattcc	aaggccttgg	600
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gcccatectc	agctgctaaa	aggaagaagc	atttttgctg	ttagcccaga	1350

1. The first step is to identify the problem or goal. This involves understanding the current situation and what needs to be achieved.

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 agattttcag gaagaaaadc acatttgtac ctttaaagcag actttagaaa 3200
 actacaggac tccaaatttt cagtcttatg acttggaacac atagactgaa 3250
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 gaaaatgagt tactaaagca ttttaataaa tacctgcctt gtaccatttt 3600
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20				25					30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn	Glu Ile Ser Trp Thr Ile	
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly	Leu Asp Lys Leu Arg Arg	
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg	Ser Ile Thr Lys Lys Ala	
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His	Leu Asp Leu Ser Asp Asn	
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala	Phe Ser Gln Met Lys Lys	
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser	Ser Leu Leu Cys Asp Cys	
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val	Ala Glu Asn Asn Phe Gln	
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His	Pro Gln Leu Leu Lys Gly	
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp	
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala	
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser	
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu	
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln	
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu	
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn	
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn	
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg	
545	550	555

Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro
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Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro
				575					580					585
Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val
				590					595					600
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser
				605					610					615
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr
				620					625					630
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp
				635					640					645
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala
				650					655					660
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser
				665					670					675
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln
				680					685					690
Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
				695					700					705
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
				710					715					720
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
				725					730					735
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
				740					745					750
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
				755					760					765
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
				770					775					780
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				785					790					795
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
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Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
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 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
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 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
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 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
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 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Pro	Arg	Phe	Asn	Arg	Ala	Leu	Phe	Asp	Pro	Leu	Leu	Val	Val	Leu
				20					25					30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
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THE **NEW** **YORK** **PUBLIC** **LIBRARY**

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Gly Gly Glu Val	Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser	Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn	590	595	600
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Ala Pro Gln Ile	Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu	Arg Arg Met His Val Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr	680	685	690
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Arg Thr Val Thr	Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala	710	715	720
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FOOTNOTES: 01001

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Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
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<210> 311

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<210> 314

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<212> DNA

<213> Homo Sapien

<400> 314

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 <211> 509
 <212> PRT
 <213> Homo Sapien

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 35 40 45
 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50 55 60
 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65 70 75
 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80 85 90
 Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95 100 105
 Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110 115 120
 Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
 125 130 135
 Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
 140 145 150
 Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155 160 165

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Pro	Arg	Phe	Arg	Gln	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Ile	Cys
				185					190					195
Lys	Cys	His	Lys	Gly	Phe	Asp	Leu	Met	Tyr	Ile	Gly	Gly	Lys	Tyr
				200					205					210
Gln	Cys	His	Asp	Ile	Asp	Glu	Cys	Ser	Leu	Gly	Gln	Tyr	Gln	Cys
				215					220					225
Ser	Ser	Phe	Ala	Arg	Cys	Tyr	Asn	Val	Arg	Gly	Ser	Tyr	Lys	Cys
				230					235					240
Lys	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Asp	Gly	Leu	Thr	Cys	Val	Tyr
				245					250					255
Ile	Pro	Lys	Val	Met	Ile	Glu	Pro	Ser	Gly	Pro	Ile	His	Val	Pro
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Lys	Gly	Asn	Gly	Thr	Ile	Leu	Lys	Gly	Asp	Thr	Gly	Asn	Asn	Asn
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Trp	Ile	Pro	Asp	Val	Gly	Ser	Thr	Trp	Trp	Pro	Pro	Lys	Thr	Pro
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Tyr	Ile	Pro	Pro	Ile	Ile	Thr	Asn	Arg	Pro	Thr	Ser	Lys	Pro	Thr
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Thr	Arg	Pro	Thr	Pro	Lys	Pro	Thr	Pro	Ile	Pro	Thr	Pro	Pro	Pro
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Pro	Pro	Pro	Leu	Pro	Thr	Glu	Leu	Arg	Thr	Pro	Leu	Pro	Pro	Thr
				335					340					345
Thr	Pro	Glu	Arg	Pro	Thr	Thr	Gly	Leu	Thr	Thr	Ile	Ala	Pro	Ala
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Ala	Ser	Thr	Pro	Pro	Gly	Gly	Ile	Thr	Val	Asp	Asn	Arg	Val	Gln
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Thr	Asp	Pro	Gln	Lys	Pro	Arg	Gly	Asp	Val	Phe	Ser	Val	Leu	Val
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His	Ser	Cys	Asn	Phe	Asp	His	Gly	Leu	Cys	Gly	Trp	Ile	Arg	Glu
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Lys	Asp	Asn	Asp	Leu	His	Trp	Glu	Pro	Ile	Arg	Asp	Pro	Ala	Gly
				410					415					420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys

425	430	435
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440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
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<210> 316
 <211> 24
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 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 316
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<210> 317
 <211> 24
 <212> DNA
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<220>
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<400> 317
 ttgcacttgt aggacccacg tacg 24

<210> 318
 <211> 50
 <212> DNA
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<220>
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<210> 319
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 <212> DNA

2007-03-27 14:20:00

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<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40				45	

His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55				60	

Pro	His	Thr	Met	Pro 65	Lys	Tyr	Leu	Leu	Gly 70	Ser	Val	Asn	Lys	Ser 75
Val	Val	Pro	Asp	Leu 80	Glu	Tyr	Gln	His	Lys 85	Phe	Thr	Met	Met	Pro 90
Pro	Asn	Ala	Ser	Leu 95	Leu	Ile	Asn	Pro	Leu 100	Gln	Phe	Pro	Asp	Glu 105
Gly	Asn	Tyr	Ile	Val 110	Lys	Val	Asn	Ile	Gln 115	Gly	Asn	Gly	Thr	Leu 120
Ser	Ala	Ser	Gln	Lys 125	Ile	Gln	Val	Thr	Val 130	Asp	Asp	Pro	Val	Thr 135
Lys	Pro	Val	Val	Gln 140	Ile	His	Pro	Pro	Ser 145	Gly	Ala	Val	Glu	Tyr 150
Val	Gly	Asn	Met	Thr 155	Leu	Thr	Cys	His	Val 160	Glu	Gly	Gly	Thr	Arg 165
Leu	Ala	Tyr	Gln	Trp 170	Leu	Lys	Asn	Gly	Arg 175	Pro	Val	His	Thr	Ser 180
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Pro	Val	Thr	Lys	Glu 200	Asp	Ile	Gly	Asn	Tyr 205	Ser	Cys	Leu	Val	Arg 210
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Tyr	Tyr	Gly	Pro	Tyr 230	Gly	Leu	Gln	Val	Asn 235	Ser	Asp	Lys	Gly	Leu 240
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Phe	Asp	Cys	Ser	Ala 260	Asp	Ser	His	Pro	Pro 265	Asn	Thr	Tyr	Ser	Trp 270
Ile	Arg	Arg	Thr	Asp 275	Asn	Thr	Thr	Tyr	Ile 280	Ile	Lys	His	Gly	Pro 285
Arg	Leu	Glu	Val	Ala 290	Ser	Glu	Lys	Val	Ala 295	Gln	Lys	Thr	Met	Asp 300
Tyr	Val	Cys	Cys	Ala 305	Tyr	Asn	Asn	Ile	Thr 310	Gly	Arg	Gln	Asp	Glu 315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu

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Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
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Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
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Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 321

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<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

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<211> 45

<212> DNA

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<223> Synthetic Oligonucleotide Probe

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<210> 324

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<212> DNA

<213> Homo Sapien

<400> 324

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atacagaaag	ttcttaattg	attttacagt	ctgtaatgct	tgatgtttta	1950
aaataataac	atttttatat	tttttaaaag	acaaacttca	tattatcctg	2000
tgttctttcc	tgactggtaa	tattgtgtgg	gatttcacag	gtaaaagtca	2050
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atagttttca	ccttaaaaga	agggggaaaa	tcataaatac	aatgaatcaa	2150
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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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20 25 30

Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys	Val Glu Glu Glu Gln Glu	
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu	Glu Ala Glu Ser Lys Glu	
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala	Ile Arg Gln Arg Ser	
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccttg gcagtcctgg tgctgttgc ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

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aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgccatacaa ctggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtcct gcaggactca gctgcagggt 500

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ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

100729-220000

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gttagctgtc tagcgcttag caagggtgct ttgtacctca ggtgttttag 2050
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cctaccagaa aaaaaaaaaa 2168

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val
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Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met
20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
200 205 210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

FOOTNOTES

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
 485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
 500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
 515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
 530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctgggta aaactgaaag 250
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<210> 339
<211> 772
<212> PRT
<213> Homo Sapien
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<400> 339
Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
          20          25          30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
          35          40          45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
          50          55          60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
          65          70          75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
          80          85          90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

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95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

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<210> 340
<211> 1572
<212> DNA
<213> Homo Sapien
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ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
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accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400
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 tttgttaaaa aaggatccat cacagccttt ctatctaggg cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
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 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile	20	25	30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	65	70	75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	95	100	105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp	125	130	135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln	155	160	165	
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr	170	175	180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys	185	190	195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln	200	205	210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val	215	220	225	
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<212> PRT

<213> Homo Sapien

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Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
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Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
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Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
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His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
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Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
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